## AMENDMENT

It is respectfully requested that the application be amended without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows[1]:

**IN THE CLAIMS**

Please amend the claims, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows:

1.      (Not Amended; Indicated As Allowed)      An isolated or purified nucleic acid molecule consisting of the nucleotide sequence set forth in Figure 1 (SEQ ID NO: 1).

2. 5.      (Thrice Amended; Indicated As Allowable If Amended As Herewith)      A primer or probe which specifically hybridizes under high stringency conditions to the nucleic acid molecule of claim 1, wherein the primer or probe consists of no more than 30 nucleotides.

3. 6.      (Twice Amended; Indicated as Allowable If Amended As Herewith)      The primer or probe of claim 5 comprising OW-216 or OW-221 (SEQ ID NOS: 3, 6), wherein the primer or probe consists of no more than 30 nucleotides.

24.      (Not Amended; Indicated As Allowed)      An isolated or purified nucleic acid molecule comprising the nucleotide sequence set forth in Figure 1 (SEQ ID NO: 1), and encoding a polypeptide having the enzymatic activity of *Candida albicans* Ess1 (CaEss1).

25.      (Not Amended; Indicated As Allowed)      An isolated or purified nucleic acid molecule consisting of a nucleotide sequence having at least 97% homology to the nucleotide sequence set forth in Figure 1 (SEQ ID NO: 1) and encoding a polypeptide having the enzymatic activity of CaEss1, wherein homology is calculated as $(N_{ref} - N_{dif})*100/N_{ref}$, wherein $N_{dif}$ is the total number of non-identical residues in the two sequences when aligned and wherein $N_{ref}$ is the number of residues in one of the sequences.

26.      (Not Amended; Indicated As Allowed)      An isolated or purified nucleic acid molecule consisting essentially of a nucleotide sequence having at least 97% homology to the nucleotide sequence set forth in Figure 1 (SEQ ID NO: 1) and encoding a polypeptide having the enzymatic activity of CaEss1, wherein homology is calculated as $(N_{ref} - N_{dif})*100/N_{ref}$, wherein

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[1] All claims now pending by this Amendment are set forth for convenient reference by the Examiner and to assist in printing. Where no amendment is desired, such is parenthetically indicated; and, the status of being allowed or allowable from the telephone conferences with George Elliot and the Examiner is also indicated parenthetically.

3

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$N_{dif}$ is the total number of non-identical residues in the two sequences when aligned and wherein $N_{ref}$ is the number of residues in one of the sequences.

     28.      (Not Amended; Indicated As Allowed)      An isolated nucleic acid molecule consisting of OW-216 (SEQ ID NO: 3).

     29.      (Not Amended; Indicated As Allowed)      An isolated nucleic acid molecule consisting of OW-221 (SEQ ID NO: 6).

     30.      (Twice Amended; Indicated As Allowable If Amended As Herewith)      An isolated nucleic acid molecule consisting essentially of OW-216 (SEQ ID NO: 3), which specifically hybridizes under high stringency conditions to the nucleotide sequence set forth in Figure 1 (SEQ ID NO: 1), wherein the isolated nucleic acid molecule consists of no more than 30 nucleotides.

     31.      (Twice Amended; Indicated As Allowable If Amended As Herewith)      An isolated nucleic acid molecule consisting essentially of OW-221 (SEQ ID NO: 6), which specifically hybridizes to under high stringency conditions the nucleotide sequence set forth in Figure 1 (SEQ ID NO: 1), wherein the isolated nucleic acid molecule consists of no more than 30 nucleotides.

     34.      (Not Amended; Indicated As Allowed)      A vector comprising the nucleic acid molecule of claim 1, 24, 25, or 26.

     Please cancel claims 3, 4, 23, 27, 32, 33 and 35-39, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, and especially without prejudice to pursuing these claims or claims otherwise subject to restriction, in one or more divisional or continuation applications.